

SID 59

RESULT 10  
E34283  
LOCUS E34283 941 bp DNA linear PAT 31-JAN-2002  
DEFINITION Environmental stress-tolerant plant.  
ACCESSION E34283  
VERSION E34283.1 GI:18624288  
KEYWORDS JP 2000116259-A/12.  
SOURCE Arabidopsis thaliana.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 941)  
AUTHORS Shinozaki, K. and Kasuga, M.  
TITLE Environmental stress-tolerant plant  
JOURNAL Patent: JP 2000116259-A 12 25-APR-2000;  
JAPAN INTERNATIONAL RESEARCH CENTER FOR AGRICULTURAL SCIENCES,  
BIO-ORIENTED TECHNOL RES ADVANCEMENT INST  
COMMENT OS Arabidopsis thaliana  
PN JP 2000116259-A/12  
PD 25-APR-2000  
PF 09-OCT-1998 JP 1998287999  
PR  
PI KAZUKO SHINOZAKI, MIE KASUGA  
PC A01H5/00, C07K14/415, C12N5/10, C12N15/09, C12P21/02// (C12N15/09,  
PC C12R1:91),  
PC (C12P21/02, C12R1:19), C12N5/00, C12N15/00, (C12N15/00, C12R1:91)  
CC  
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Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 632 ATATCATACCGACATCAGTT 651

RESULT 11  
E34339  
LOCUS E34339 941 bp DNA linear PAT 31-JAN-2002  
DEFINITION Environmental stress-tolerant plant.  
ACCESSION E34339  
VERSION E34339.1 GI:18624324  
KEYWORDS JP 2000116260-A/12.  
SOURCE Arabidopsis thaliana.  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 941)  
AUTHORS Shinozaki,K. and Kasuga,M.  
TITLE Environmental stress-tolerant plant  
JOURNAL Patent: JP 2000116260-A 12 25-APR-2000;  
JAPAN INTERNATIONAL RESEARCH CENTER FOR AGRICULTURAL SCIENCES,  
BIO-ORIENTED TECHNOL RES ADVANCEMENT INST

COMMENT OS Arabidopsis thaliana  
PN JP 2000116260-A/12  
PD 25-APR-2000  
PF 14-OCT-1998 JP 1998292348  
PR  
PI KAZUKO SHINOZAKI,MIE KASUGA  
PC A01H5/00,C07K14/415,C12N15/09,C12N15/00  
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FH Key Location/Qualifiers  
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FEATURES Location/Qualifiers  
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Db 632 ATATCATACCGACATCAGTT 651

RESULT 12  
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LOCUS ATLTI78 3420 bp DNA linear PLN 16-MAR-1993  
DEFINITION A.thaliana lti78 gene.  
ACCESSION X67671  
VERSION X67671.1 GI:16389  
KEYWORDS lti78 gene.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 3420)  
AUTHORS Vahala,T.K.  
TITLE Direct Submission  
JOURNAL Submitted (10-AUG-1992) T.K. Vahala, Swedish Univ. of Agricultural  
Sciences, Dept. of Molecular Genetics, Box 7003, 75007 Uppsala,  
SWEDEN

REFERENCE 2 (bases 1 to 3420)  
AUTHORS Nordin,K., Vahala,T. and Palva,E.T.

TITLE Differential expression of two related, low-temperature-induced  
 genes in *Arabidopsis thaliana* (L.) Heynh  
 JOURNAL Plant Mol. Biol. 21 (4), 641-653 (1993)  
 MEDLINE 93192524  
 FEATURES

	Location/Qualifiers
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misc_feature	740. .747 /note="ABA-responsive element, putative"
TATA_signal	770. .775 /note="putative"
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exon	1018. .1200 /gene="lti78" /number=2 /evidence=experimental
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Db      574 ATATCATACCGACATCAGTT 593

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RESULT 13
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DEFINITION Arabidopsis thaliana cor78 protein gene, complete cds.
ACCESSION  L22568
VERSION    L22568.1  GI:404667
KEYWORDS   cor78 gene.
SOURCE     Arabidopsis thaliana DNA.
  ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 3533)
  AUTHORS  Horvath,D.P., McLarney,B.K. and Thomashow,M.F.
  TITLE    Cor78 genomic sequence
  JOURNAL  Unpublished (1993)
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BASE COUNT 1168 a 564 c 848 g 953 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 577 ATATCATACCGACATCAGTT 596

RESULT 14

D13044

LOCUS D13044 8048 bp DNA linear PLN 14-APR-2000

DEFINITION Arabidopsis thaliana DNA for RD29B, RD29A, complete cds.

ACCESSION D13044

VERSION D13044.1 GI:285614

KEYWORDS RD29A; RD29B.

SOURCE Arabidopsis thaliana (strain:Columbia) DNA.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (sites)

AUTHORS Yamaguchi-Shinozaki,K. and Shinozaki,K.

TITLE Arabidopsis DNA encoding two desiccation-responsive rd29 genes

JOURNAL Plant Physiol. 101 (3), 1119-1120 (1993)

MEDLINE 94143472

REFERENCE 2 (bases 1 to 8048)

AUTHORS Shinozaki, K.

TITLE Direct Submission

JOURNAL Submitted (25-AUG-1992) Kazuo Shinozaki, Tsukuba Life Science Center, The Institute of Physical and Chemical Research; 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
(E-mail:sinozaki@rtc.riken.go.jp, Tel:0298-36-4359, Fax:0298-36-9060)

FEATURES

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exon	2222. .2736 /gene="rd29B" /number=3
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TATA_signal	5398. .5403
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 ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 8048;  
 Best Local Similarity 100.0%; Pred. No. 4.1;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15  
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 LOCUS AB019226 73999 bp DNA linear PLN 27-DEC-2000  
 DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K24M7.  
 ACCESSION AB019226 BA000015  
 VERSION AB019226.1 GI:3869065  
 KEYWORDS .  
 SOURCE Arabidopsis thaliana (strain:Columbia) DNA, clone\_lib:Mitsui TAC  
 clone:K24M7.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (sites)  
 AUTHORS Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E., Kotani,H.  
 and Tabata,S.  
 TITLE Structural analysis of Arabidopsis thaliana chromosome 5. X.  
 Sequence features of the regions of 3,076,755 bp covered by sixty  
 P1 and TAC clones  
 JOURNAL DNA Res. 7 (1), 31-63 (2000)  
 MEDLINE 20181125  
 REFERENCE 2 (bases 1 to 73999)

AUTHORS Nakamura, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp, Tel: 81-438-52-3935, Fax: 81-438-52-3934)

COMMENT Address for correspondence: kaos@kazusa.or.jp  
 For the latest information on annotation of this clone, please see [http://www.kazusa.or.jp/kaos/cgi-bin/agd\\_graph.cgi?c=K24M7](http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=K24M7)  
 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.  
 The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/Grail-1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and SplicePredictor (Volker Brendel, Stanford University, <http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi>).  
 Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).  
 This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.  
 The 5' clone is F17P19 and the 3' clone is T4M5.

FEATURES

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SRETHHESLNTPVSLLSGTEDVTSTFAPSGDDEYLDGQRKVNVEPITLEESAVSDY  
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APLGGNFPVRSHDLK NESDIDKDVPTGFDGEPDFLAKGRPGYGEASEEDKFPARSD  
DVEVETELGRDPKTETLDQFSPELSHPKERDEFKESRDDFEETRDEKTEEPKQSTYTE  
KFASMLGYSGEIPVGDQTVAGTVDEKLTPVNEKDQETESAVTTKLPISGGGSGVEEQ  
RGEDKSVSGRDYVAEKLTTTEEDKAFSDMVAEKLQIGEEEEKETTTKEVEKISTEKA  
ASEEGEAVEEEVKGGGMVGRIKGFVGGGATDEVKPESPHSVVEEAPKSSGWFVGGGATE  
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CDS complement(16832. .18340)

/note="gene\_id:K24M7.5"

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21124. .21235,21423. .21453))
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gb|AAB70446.1
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LSKLEDEFRQILQYNSKPMEPDRLFECPLPSNLRPSSEGE GGGGKTHDPHKSLENAIF
TVPTVIPPRVLP LLHDLAQQM VQAGHQQLFKSYRDTRA AVLEQSLRKLGVRLSKDD
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CDS join(26632. .26954,27047. .27277,27393. .27531,27629.
.27841,
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LPVLHDLAQQMVKAGHQQELFKTYRDIRRAVLAQSLEKLGVERHSKYDVERMNQDVFE  
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Query Match 100.0%; Score 20; DB 8; Length 73999;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atatcataccgacatcagtt 20  
||||||||||||||||  
Db 12340 ATATCATACCGACATCAGTT 12359

RESULT 10

AAA53425

ID AAA53425 standard; DNA; 941 BP.

XX

AC AAA53425;

XX

DT 04-OCT-2000 (first entry)

XX

DE Rd29A gene fragment nucleotide sequence.

XX

KW Dehydration responsive element; DRE; transgenic plant; stress; salinity;

KW environmental stress; temperature; stress resistant plant; PCR primer;

KW rd29A; ds.

XX

OS Arabidopsis thaliana.

XX

PN JP2000116260-A.

XX

PD 25-APR-2000.

XX

PF 14-OCT-1998; 98JP-0292348.

XX

PR 14-OCT-1998; 98JP-0292348.

XX

PA (NORQ ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO.

PA (SEIB-) SEIBUTSUKAI TOKUTEI SANGYO GIJUTSU.

XX

DR WPI; 2000-389819/34.

XX

PT New transgenic plants resistant to environmental stresses, comprise a

PT DNA bound with a gene encoding for a transcription factor in a stress

PT responsive promoter -

XX

PS Example 5; Page 26; 36pp; Japanese.

XX

CC This invention relates to transgenic plants that are resistant to  
CC environmental stresses. This sequence represents a fragment of an rd29A  
CC gene used in the production of the transgenic plants of the invention.

CC The transgenic plants comprise a vector containing a gene encoding a  
CC transcription factor and a stress responsive element (e.g. DRE

CC dehydration responsive element or rd29A promoter sequence). The

CC transcription factor gene is linked to the stress responsive element.

CC Also included in the invention is a method for the preparation of the

CC transgenic plants. This method can be used to prepare stress resistant

CC agricultural plants, which are resistant to dehydration, low temperature

CC and salinity.

XX

SQ Sequence 941 BP; 372 A; 144 C; 140 G; 285 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 941;

Best Local Similarity 100.0%; Pred. No. 0.57;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atatcataccgacatcagtt 20

|||||

Db 632 atatcataccgacatcagtt 651

RESULT 11

AAA53474

ID AAA53474 standard; DNA; 941 BP.

XX

AC AAA53474;

XX

DT 04-OCT-2000 (first entry)

XX

DE Rd29A promoter nucleotide sequence.

XX

KW Dehydration responsive element; DRE; transgenic plant; stress; salinity;

KW environmental stress; temperature; stress resistant plant; rd29A;

KW promoter; ss.

XX

OS Arabidopsis thaliana.

XX

PN JP2000116259-A.

XX

PD 25-APR-2000.

XX

PF 09-OCT-1998; 98JP-0287999.

XX

PR 09-OCT-1998; 98JP-0287999.

XX

PA (NORQ ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO.

PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.

XX

DR WPI; 2000-379177/33.

XX

PT Plants resistant to environmental stresses. -

XX

PS Example 5; Page 26; 36pp; Japanese.

XX

CC The invention relates to transgenic plants resistant to environmental  
 CC stress. The plants comprise a vector containing a gene downstream of a  
 CC stress responsive element e.g. the stress responsive promoter of rd29A or  
 CC a dehydration responsive element (DRE). Also included in the invention is  
 CC a method for the production of the transgenic plants. This method can be  
 CC used to prepare stress resistant agricultural plants, which are resistant  
 CC to dehydration, can withstand low temperatures and environments of high  
 CC salinity.

CC The present sequence represents the promoter of the rd29A gene. The PCR  
 CC product is used in the production of the plants of the invention.

XX

SQ Sequence 941 BP; 372 A; 144 C; 140 G; 285 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 941;

Best Local Similarity 100.0%; Pred. No. 0.57;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atatcataccgacatcagtt 20

|||||

Db 632 atatcataccgacatcagtt 651